

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1 - 5. (Canceled)

6. (Previously presented) The method of claim 8, wherein the DNA methylation pattern for the test cell, test tissue, or test nucleus and the differentiation state-specific DNA methylation pattern each comprise information on the methylation state of at least about 1,000 gene regions.

7. (Canceled)

8. (Currently amended) A method of identifying the differentiation state of a test cell, test tissue, or test nucleus, wherein the test cell, test tissue, or test nucleus is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, and a differentiating stem cell nucleus, wherein the differentiating stem cell, the differentiating stem cell tissue, and the differentiating stem cell nucleus are not differentiated, comprising:

obtaining a DNA methylation pattern for the test cell, test tissue, or test nucleus, wherein the DNA methylation pattern for the test cell, test tissue, or test nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a differentiation state-specific DNA methylation pattern for one or more cell, tissue, or nucleus of known differentiation state, wherein the one or more cell, tissue, or nucleus of known differentiation state is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, and a differentiating stem cell nucleus, wherein the differentiating stem cell, the differentiating stem cell tissue, and the differentiating stem cell nucleus are not differentiated; and,

comparing the DNA methylation pattern for the test cell, test tissue, or test nucleus with the differentiation state-specific DNA methylation pattern,

wherein the differentiation state of the test cell, test tissue, or test nucleus is identified if the DNA methylation pattern of the test cell, test tissue, or test nucleus matches the differentiation state-specific DNA methylation pattern.

9. (Previously presented) The method of claim 8, wherein the DNA methylation patterns are obtained by generating RLGS profiles.

10 - 18. (Canceled)

19. (Previously presented) The method of claim 8, wherein the test cell, test tissue, or test nucleus is an embryonic stem cell, embryonic stem cell tissue, embryonic stem cell nucleus, differentiating embryonic stem cell, differentiating embryonic stem cell tissue, or differentiating embryonic stem cell nucleus.

20. (Canceled)

21. (Previously presented) The method of claim 8, wherein the differentiation state of the one or more cell, tissue, or nucleus of known differentiation state is undifferentiated.

22. (Currently amended) A method of identifying a test cell, test tissue, or test nucleus, wherein the test cell, test tissue, or test nucleus is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, and a differentiating stem cell nucleus, wherein the differentiating stem cell, the differentiating stem cell tissue, and the differentiating stem cell nucleus are not differentiated, comprising:

obtaining a DNA methylation pattern for the test cell, test tissue, or test nucleus, wherein the DNA methylation pattern for the test cell, test tissue, or test nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a cell-, tissue-, or nucleus-specific DNA methylation pattern for one or more known types of cell,

tissue, or nucleus; wherein the one or more known types of cell, tissue, or nucleus is selected from undifferentiated embryonic stem cell, differentiating embryonic stem cell, undifferentiated trophoblast stem cell, and differentiating trophoblast stem cell, wherein the differentiating embryonic stem cell and the differentiating trophoblast stem cell are not differentiated; and,

comparing the DNA methylation pattern for the test cell, test tissue, or test nucleus with the cell-, tissue-, or nucleus-specific DNA methylation pattern of the known cell, tissue, or nucleus to permit identification of the test cell, test tissue, or test nucleus as one of the known types of cell, tissue, or nucleus;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated embryonic stem cell identifies the test cell, test tissue, or test nucleus as undifferentiated embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the differentiating embryonic stem cell identifies the test cell, test tissue, or test nucleus as differentiating embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated trophoblast stem cell identifies the test cell, test tissue, or test nucleus as undifferentiated trophoblast stem cell; and

wherein a match to the cell-, tissue-, or
nucleus-specific DNA methylation pattern of the
differentiating trophoblast stem cell identifies the
test cell, test tissue, or test nucleus as differentiating
trophoblast stem cell.

23. (Previously presented) The method of claim 22, wherein the DNA methylation
patterns are obtained by generating RLGS profiles.

24. (Previously presented) The method of claim 8, wherein the
differentiation state of the one or more cell, tissue, or nucleus of known
differentiation state is differentiating.